

Fig 1

Consensus	X_n	-D-	X_n	-EE-	X_n	-DPiDgt-	X_n	-wd-	X_{11}	-GG-	X_n
	47		70		90		219		232		
Impase1	X_{46}	-D-	X_{22}	-EE-	X_{18}	-DPIDGT-	X_{123}	-WD-	X_{11}	-GG-	X_{57}
	54		79		153		315		328		
1ptase	X_{53}	-D-	X_{24}	-EE-	X_{72}	-DPIDST-	X_{156}	-WD-	X_{11}	-GG-	X_{70}
	75		98		119		280		293		
Fbpase1	X_{74}	-D-	X_{22}	-EE-	X_{19}	-DPLDGS-	X_{155}	-YE-	X_{11}	-GG-	X_{44}

Fig 2

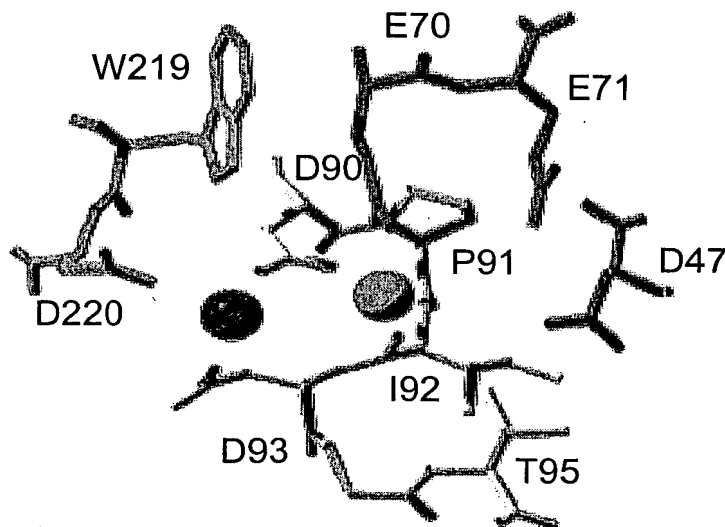




Fig 4

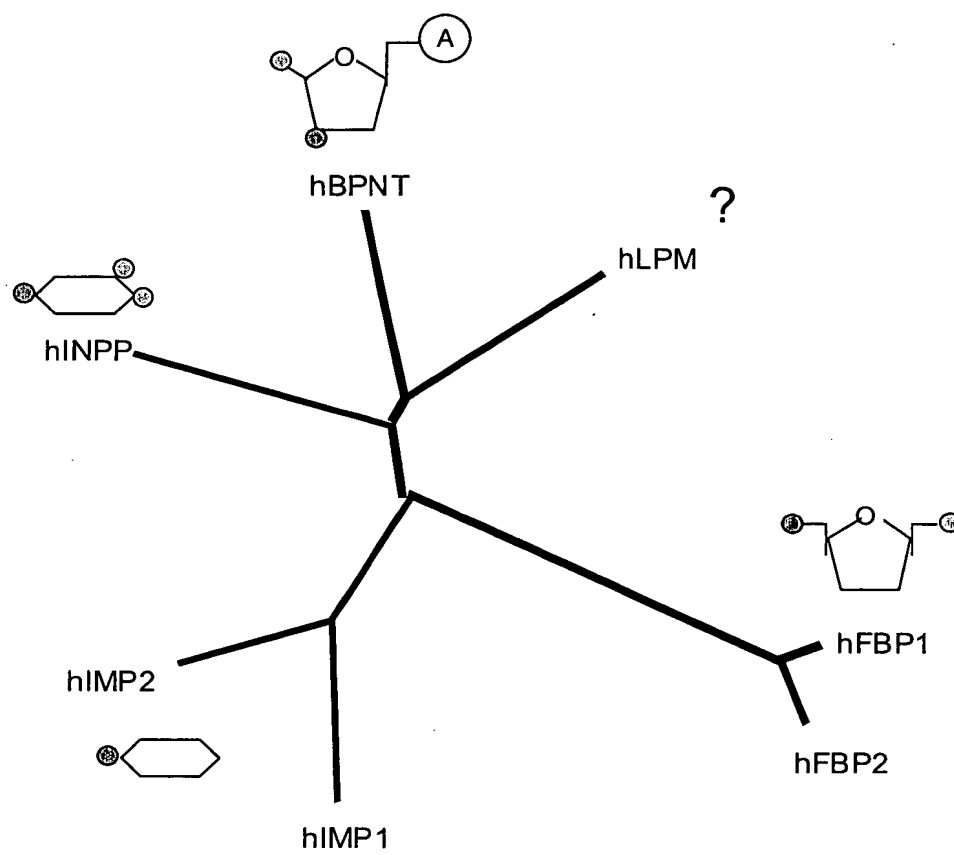


Fig 5

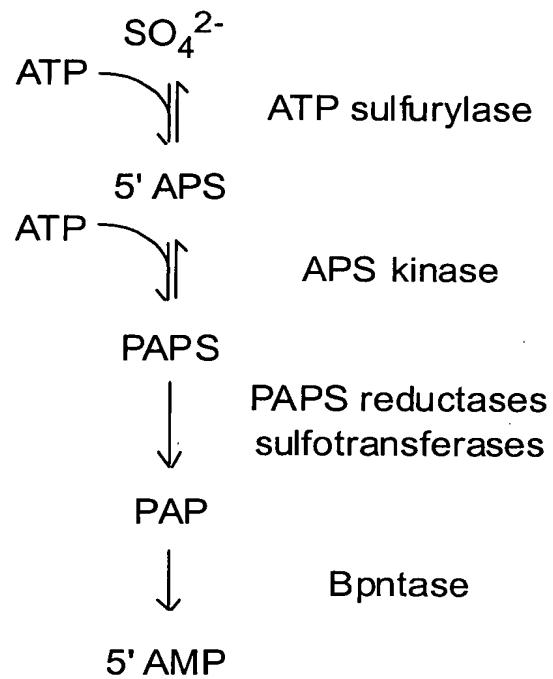


Fig 6

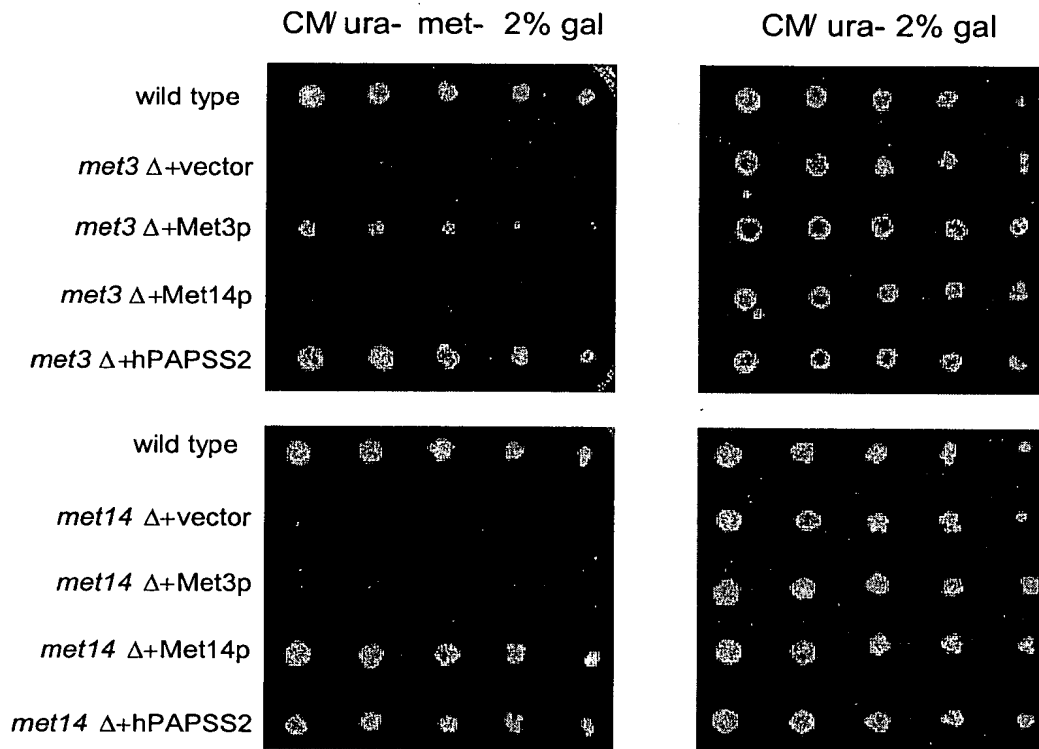


Fig 7

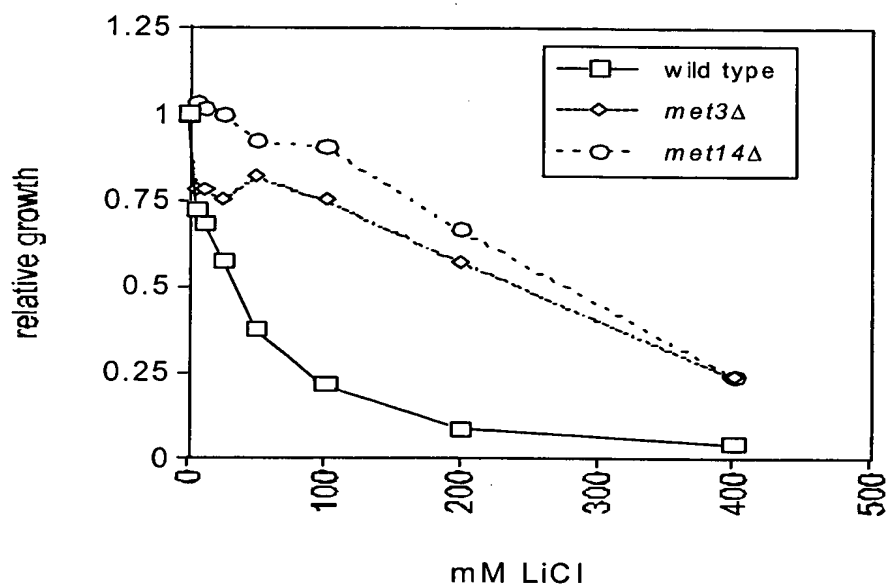


Fig 8

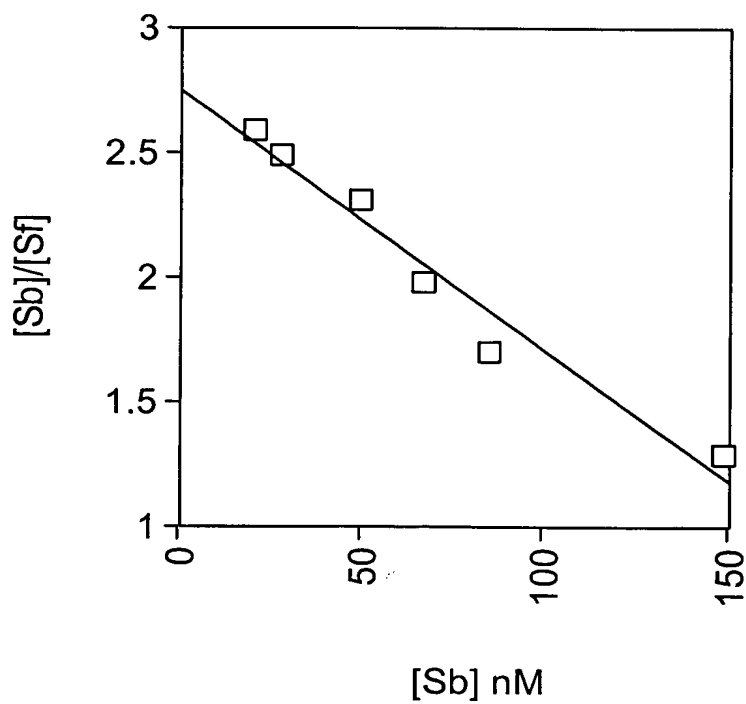


Fig 9

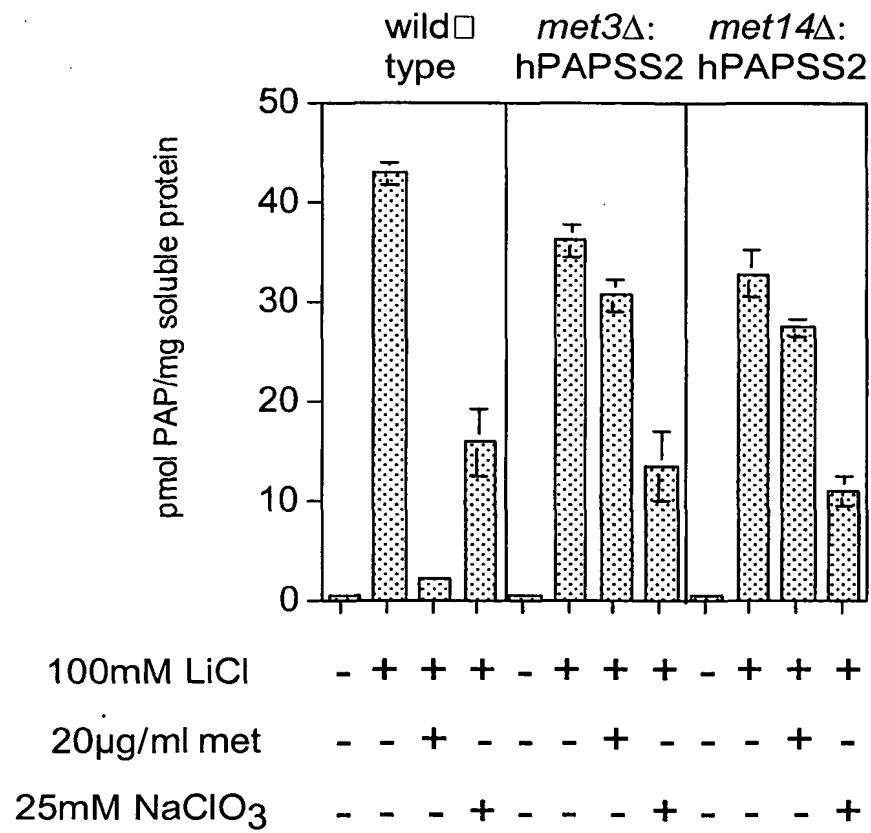


Fig 10

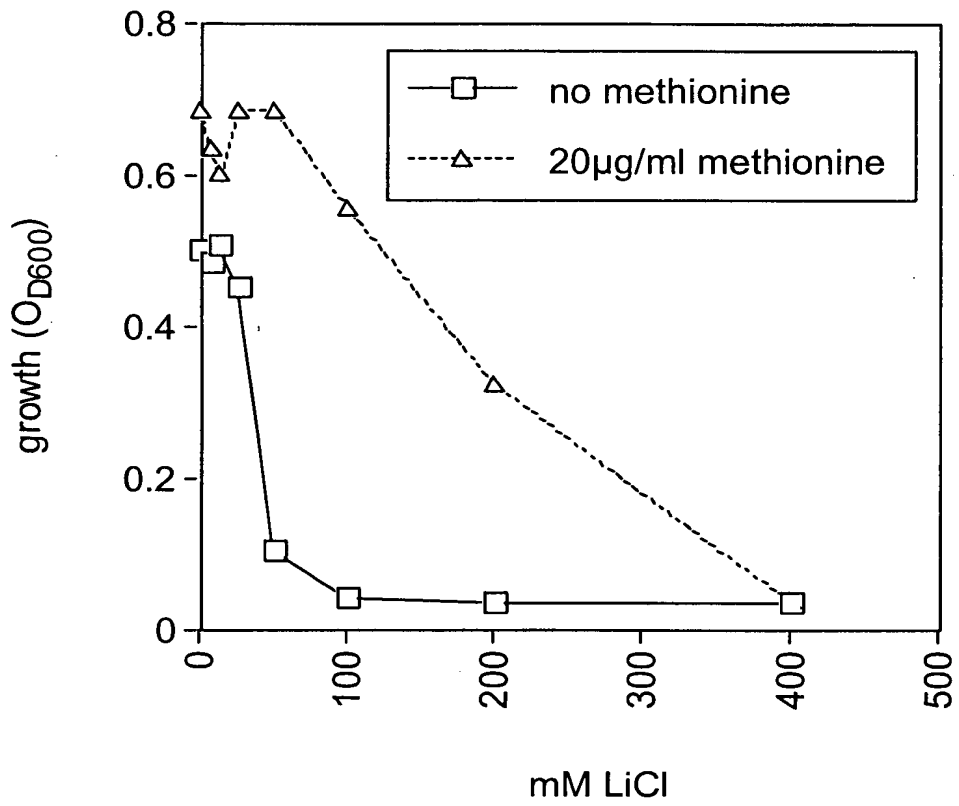


Fig 11

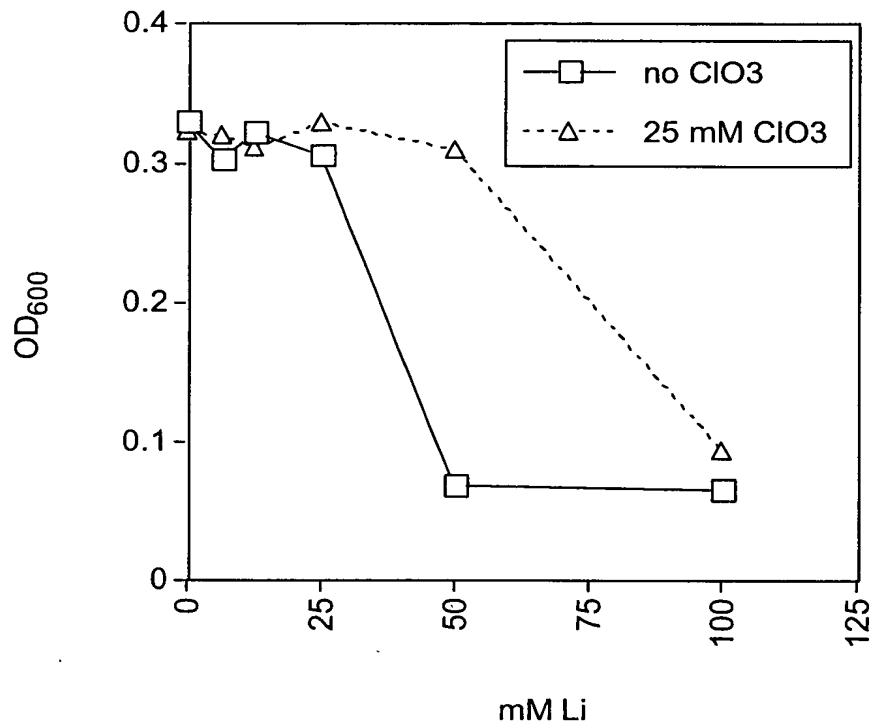


Fig 12

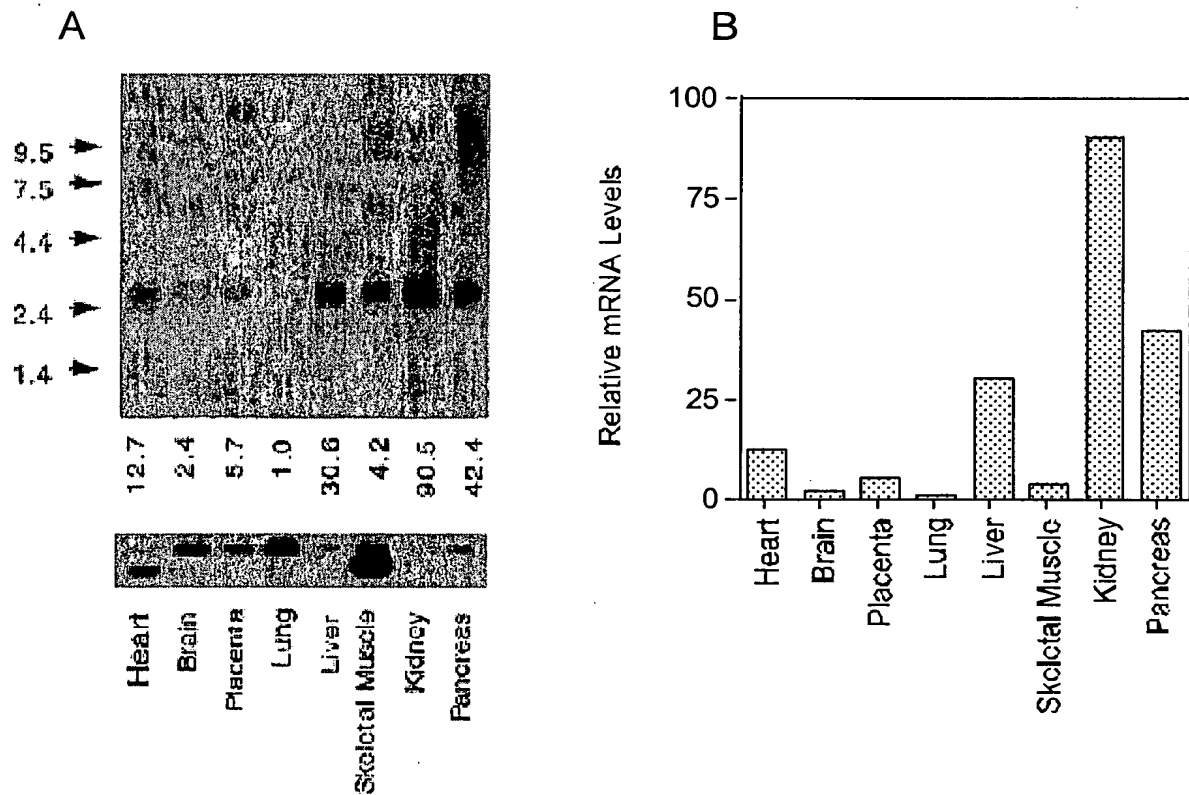


Fig 13

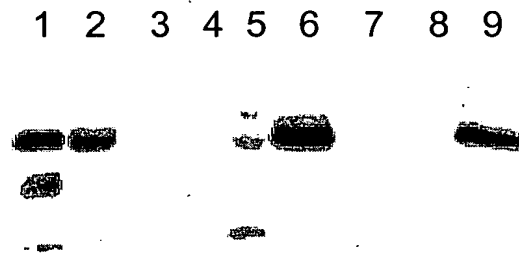


Fig 14

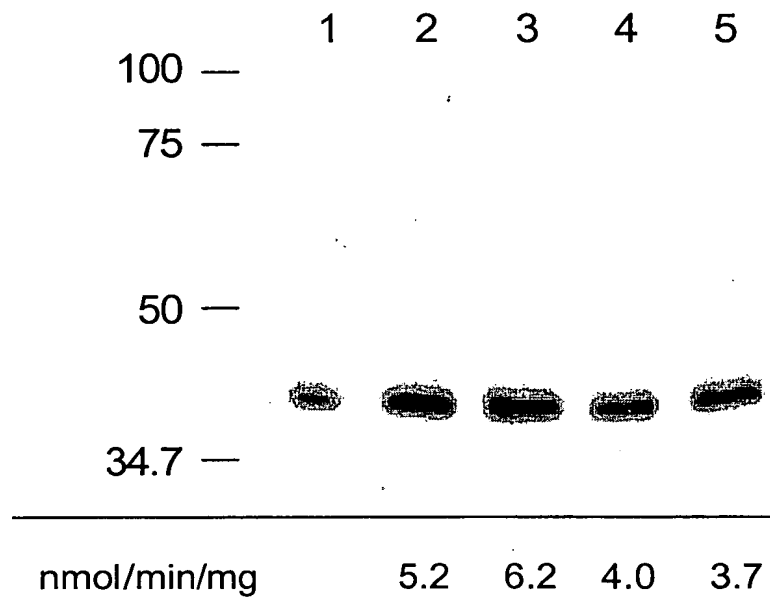


Fig 15

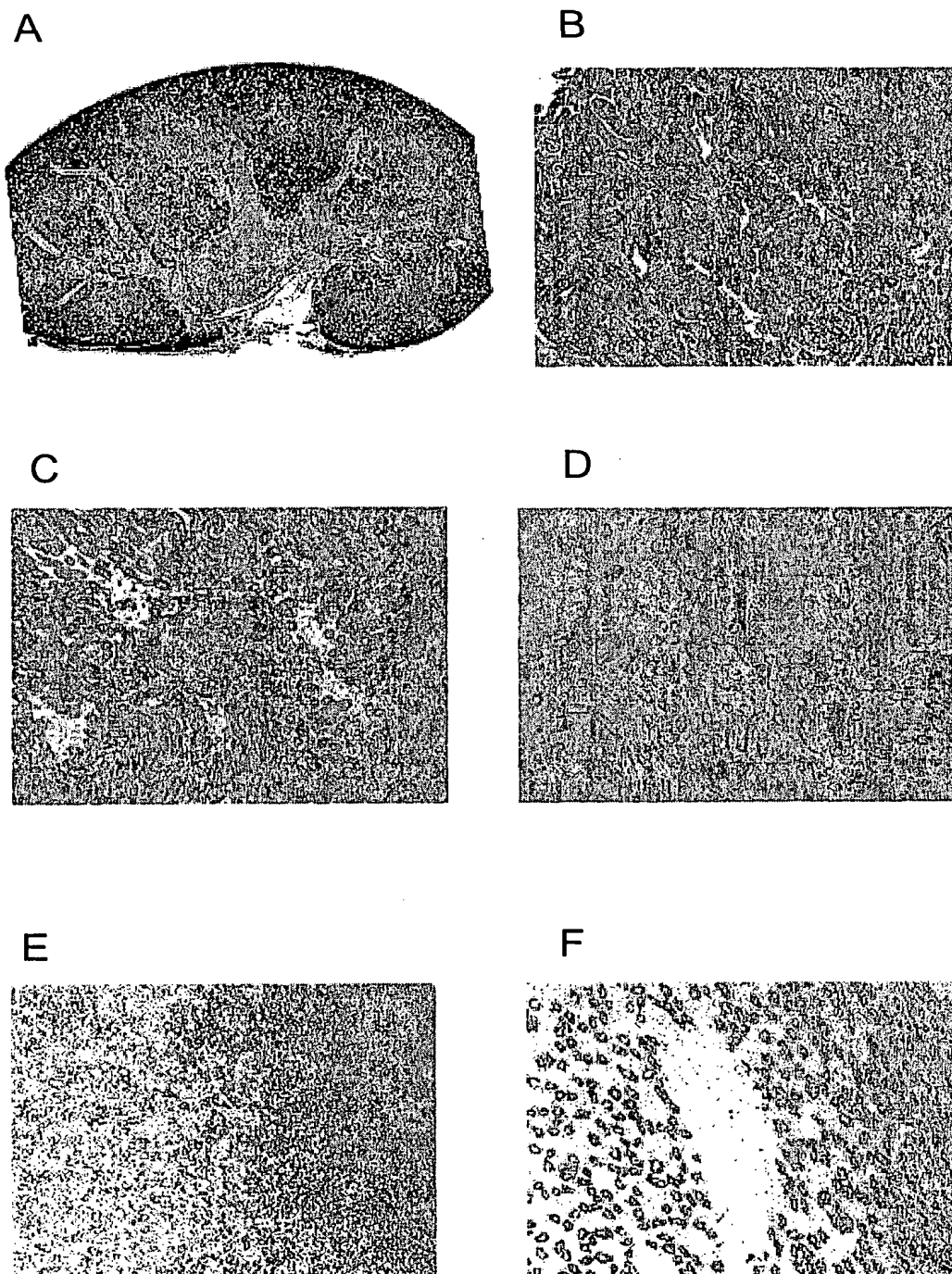
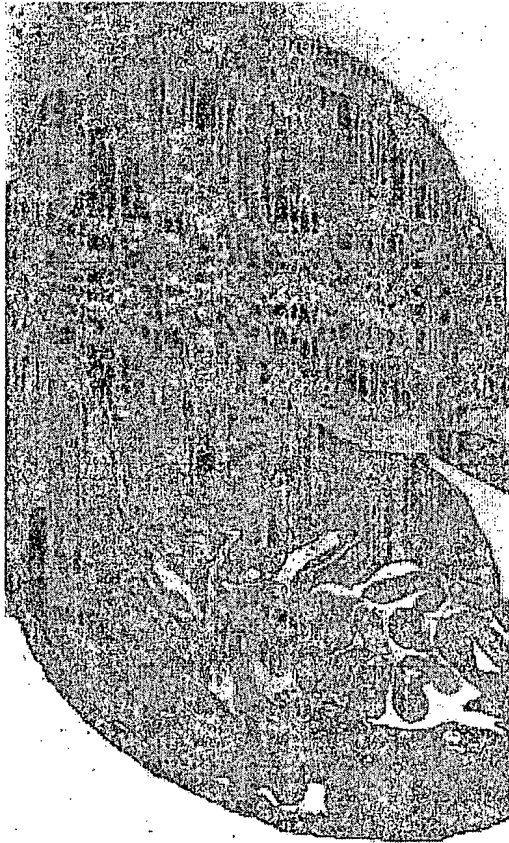


Fig 16

A



B



Fig 17

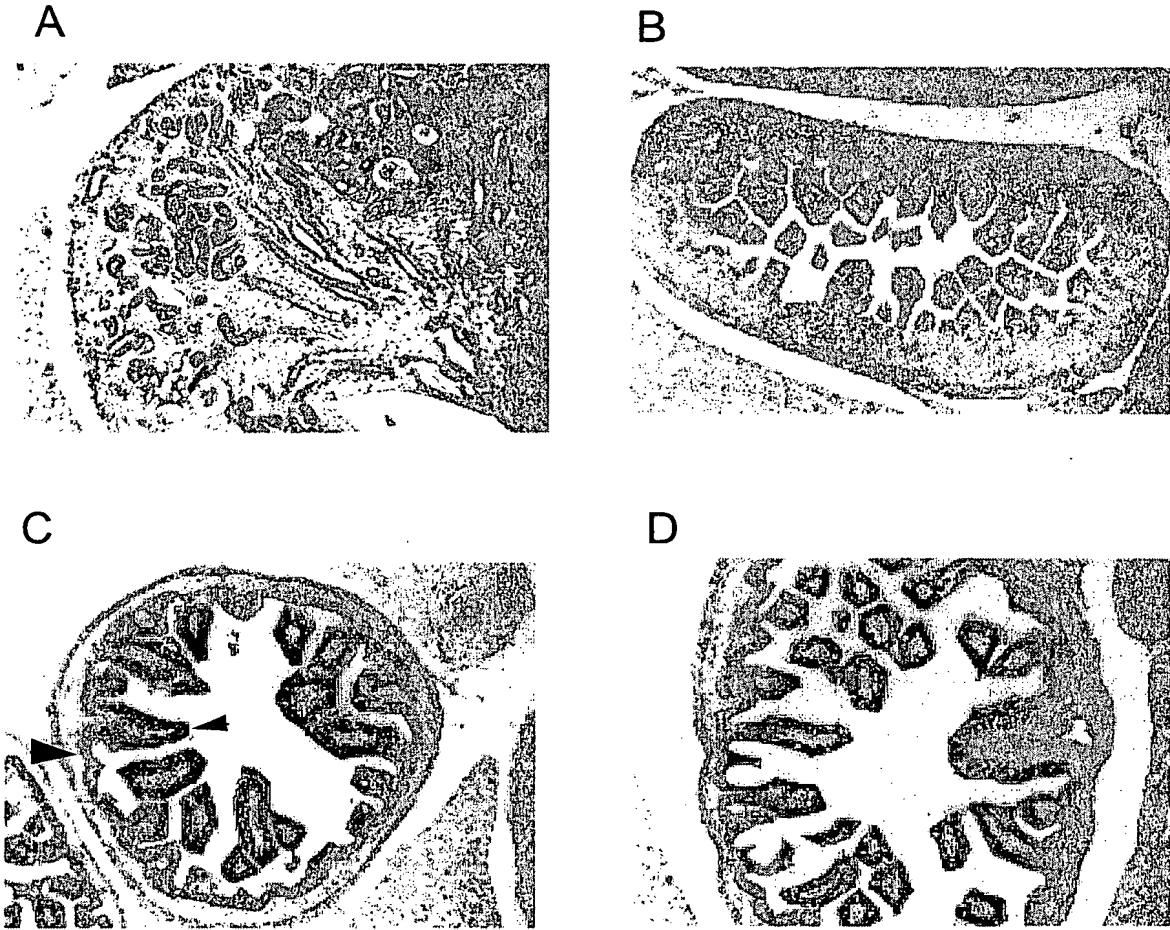


Fig 18

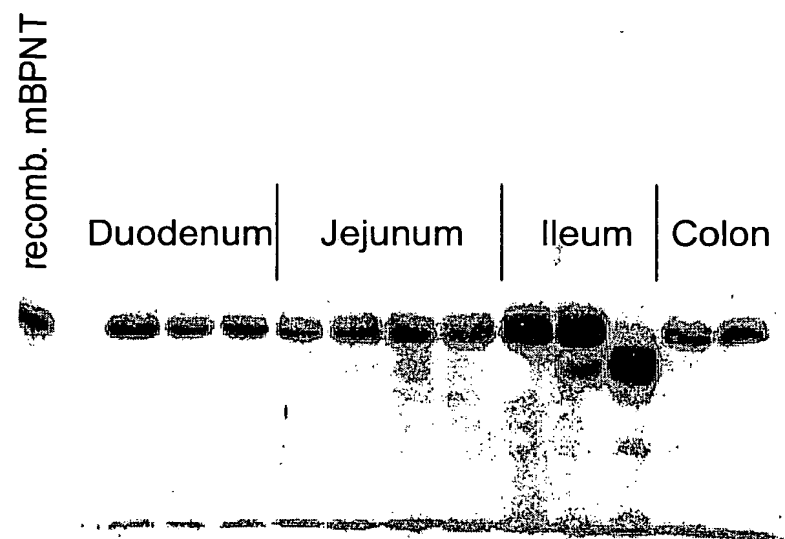


Fig 19

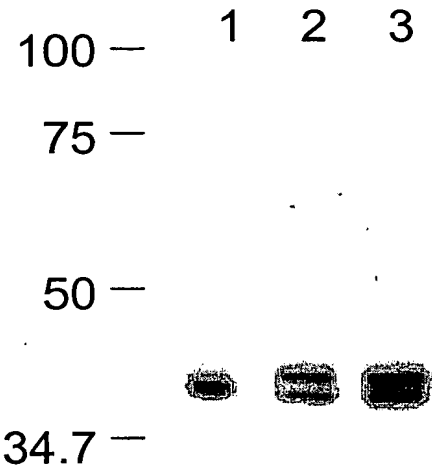
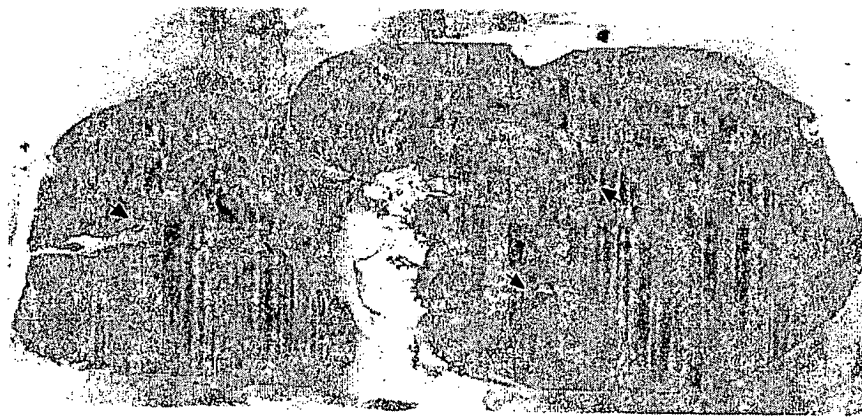
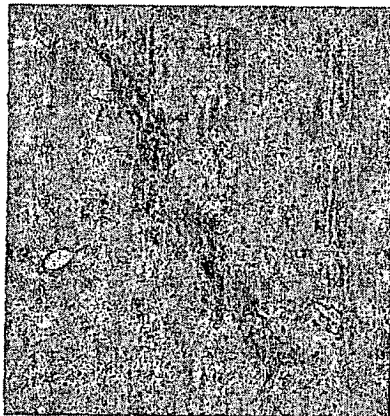


Fig 20

A



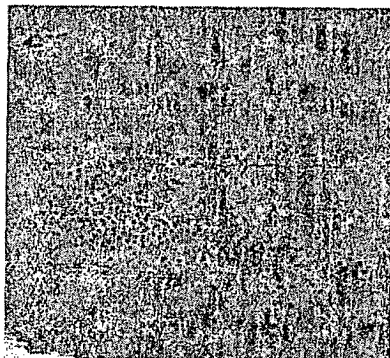
B



C



D



E

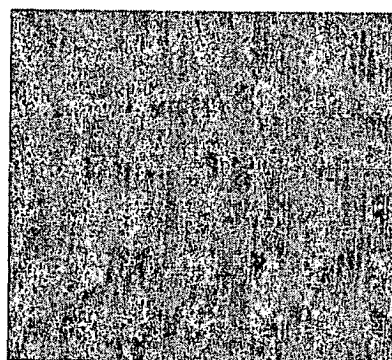


Fig 21

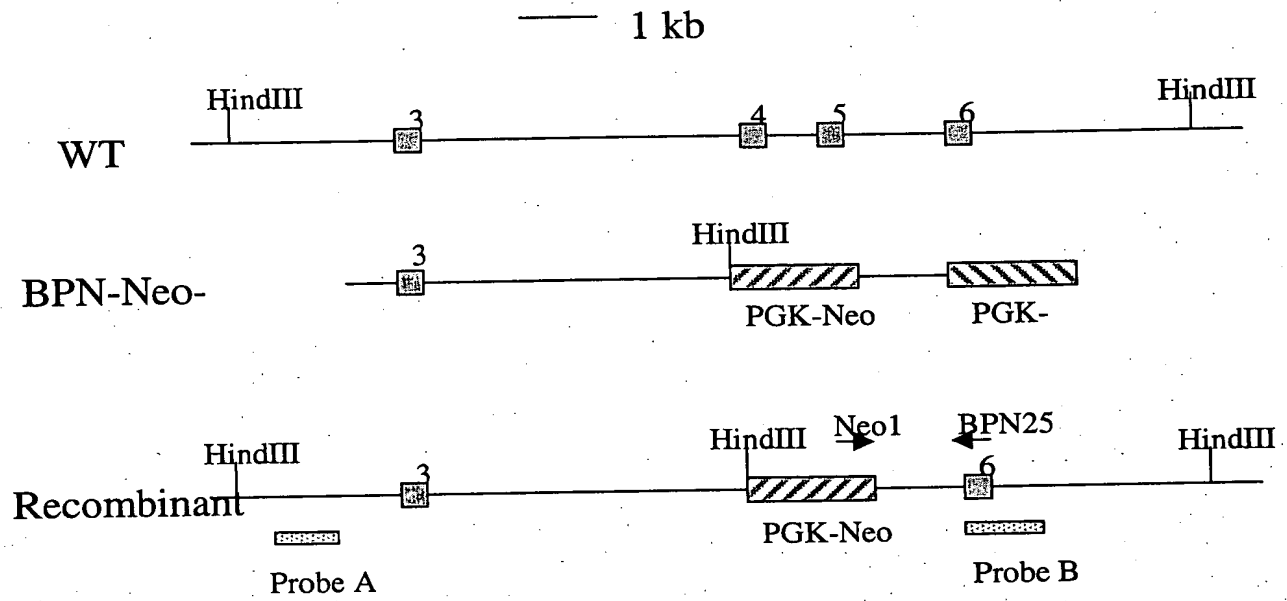


Fig 22A

1	10	20	30	40	50	60	70	80	90	100
1	TGGCGAGCTT	GCTTATTCTG	CTTTTCAGAGT	ATGGGGTGT	ATAAAGCAGC	TGGCGGCACA	CTGGGGTTTC	CCGACTCTTA	GCCCATTTAA	AGCAGGTTGG
101	AATCTAGAGC	GTTATGAAAG	AGTTTCTCAA	TTAGAGAAGA	GAATATTCCA	AATAATTAA	AAGCACCTTT	GCAAACTTGA	ACTGTTGTGG	AGCTGGGAAT
201	CGAGTTCAGT	GGTAGTGCCT	GCTTGGTGTG	TGTCAGGGGC	GTGTGTGATC	TCTATCAGCA	CACACACACA	CACACACAGC	CACGACGCA	CGCACACACA
301	CACGCACGCA	CACACACAGC	CACACACGCA	CGCACACAGC	CGCGCACACA	CACACACACA	CACACACACA	CACACACGCT	GTTTTAAACT	ATGATTGTTT
401	ATTGGTATAC	AGTTTCACAC	GGTAGTACAA	GCTGATCTCA	GATTTCATGGC	TGTCCTTCTA	TGTCCTGATA	TTAGAGCCGT	GCAGTGCTAT	CCAGCCTCAC
501	TTCTCAGTCT	TTTTTGTGTT	TTGTTTTGTT	TTGTTTTGTT	TTGTTTTATT	TTTTTGAGAC	AGGGTTTCTC	TGTGAAGCCC	TGGCTGTCTT	GGAACTCACT
601	CTGTAGACCA	GGCTGGCCTC	GAATCAGAA	ATCCGCTGCG	CTCTGCCTCC	CGAGTGTCTG	GATTAAGAGC	GTGCGCCGCG	ACGCCCCGGC	TCACTTCTCA
701	GTCTTAGCTG	CTGTTACTTC	TCTGAGAAGC	AGCGAGGGCC	CTGACTAGTT	GATCCCTGGG	CTCGGGTCTG	CGTTATAGTG	GGGAGTCGGA	AGACTGGTTA
801	CCCCGATTTG	TACTGATACG	GAGATTTGCA	TTCTTGTTTA	CAGACCTCGG	CCACCGACCT	CGAGACCAAA	GCCGACCCGT	TGGTGCAGAT	GAGCATATGC
901	TCTTCCCTGG	CCCGAAGTT	CCCGAAGCTG	ACCATATGAG	GGGAAGAGGT	GAGAGGCGCG	CGCCACTTGG	ATTCATACCC	TACCTGCCAT	TGAGCCGTAG
1001	GTTATGGTCA	GTCTTAGCGT	TGGCACTAAC	GTTCACACAC	AAAGCGATCG	TTTTCTTAG	GGGAAAAATC	TGACTTAATG	ATATTTTGGT	CCACTTAATG
1101	GGCTAAGTCT	CCATTTCTAG	TGATGGGAGC	TATGGTCACC	ATTGTAATAC	CATACGATGG	ACTCAGTGGC	AGAAAGTCGC	CTACTGTATG	TGAGGCTCTA
1201	AGGTGGGAGA	CATCTCAGTC	ATAAGACCAT	GTGGCTCACA	TATGTATGAT	CTCGGGTTGG	AGCCCCGTGA	TCAGCAGTTA	TATGTGAAGA	GTGCGCAAGG
1301	TTCTGGAACT	CTGAGATGAC	TGGGCTTGGT	TGCTGTGCT	GCTTGTCCGT	CATTTCAGAT	TGGACTTGTG	TACTTACAA	TGAACAATA	GACTATGTTT
1401	TAGTTTTGTT	TTTTATTAAG	TAGTTTCGTT	GACAATTAG	TGCATACATG	TATACATCTT	TGATTTCCCT	CATACTTCGG	ATTCCTCTCC	CCTCCCTTCC
1501	TTCTTGGCCC	GGCCCTCTTT	CCCCTTAGT	TTATTCAGGA	TCATCCATGT	GACCATTTCA	TTGGGACCAT	CCATTGGTCA	TCAGTGGTGC	ACAGTGGTAA
1601	GCAATGGCTT	CCCCCTTCCC	TGAATCAGTC	TGTAGGAAAT	AGTTTCTGAG	TGAAGGAGAG	AGAGTGTCTG	TCTGCATCTC	TCTCTCCACT	CTGCTTAACT
1701	GTGGGACTG	ATCTTCTCTC	AGACCCAGCA	CAGTCATCCG	GTGTGTGAGA	GTTACGCTCT	GCAGCTGGCT	GCACCCGAGT	TAATGACGTT	GGCAGGCTTT
1801	CTCCCGTTT	TTACGCTCTT	ACCATCTTTC	TGCCCTCTCT	CTACAAGGCC	TGGTAAACCT	TAGAGGGGAT	AAATGTCTAA	ATATCTTATT	CAGAGCTGAG
1901	CAATCAGCTG	TAGTTTGTCT	TTATTAGGCC	TTCATATATC	TCTCCCTTCA	TTATAGTCTT	CTAGAAGAG	AATCTTCTCT	GACTAAGGCT	GAGTGGTAAT
2001	TCGCTATGTT	AAATAACATC	TATATTTAGG	AAGCTGTTTG	ACACTGTGTG	ACTTTAGTAA	AGCTGTAGAG	TTTAACCTCC	TAAGAGGACT	CATGGCTCTC
2101	CTTTTATATC	ACTGAGTGGG	TCTCCAGACA	TGGAGTGTGT	TTAACGTACT	AAGCGTGGAT	TCCCATGCTG	GAGTAGCCCT	CACATTCGAT	CAAGAGCAGG
2201	TAGTTACCCC	CCAAACAGTC	CGACACTGTT	GTGTGATGCT	TGAGCACAGC	TTGCTGACA	GATGGTGCTG	TAGTTGTCTA	GGTGACAGA	TGCGCAATAC
2301	TTCTTCCCC	AGCAGCCTGC	AGAGAAAATG	TGTTCAAGTC	TGACTTCTTT	GTCTCATGCA	ACCAAGTGT	GTGGTGTCAT	TAGCAGTAAG	GTCTTAGCAT
2401	CTAATGCTAG	TGGGCAACCA	AGAAAAATGA	CAATGCCTAT	ATTGTCTTAG	GGCAGTGGGA	CCTCCGTGAC	CAACTTATCA	GGAGGCACCA	CACACACAGC
2501	AGGTGGGGTT	TTAATGAAGG	ATAATTTTCA	AGGGGAGCAG	TTTCTAGGTC	TCTCTCTTCC	AACCTAAAAA	AATGCATCCT	AGTTATTGTG	AGTAAATTTA
2601	AAATCAACAG	ATAAGTTAGT	TTCCAACAGT	GCGATGTGAG	GCCTCTGGAC	GTGTGGAAAG	CAGCAGTATT	CCATGTACTG	GAGTAGCTGG	CCATGTGCCG
2701	GAACAGCTGG	GCTACGGATG	CTGTTCTTAG	TGTTGTAAGG	AATTGCCACA	CCAGTTTCCA	TATGGCTGCA	CTGGTTTCCC	ACCAGCAATG	AAGGAGTCCC
2801	TCTTTTCCAC	CCTCACCAGC	ACTGCCTGTC	TTGAGGTTTC	TTACGGATTG	CCATTCTGAC	AGGACAAGAT	GAAATCTTAG	AGCAGCTTTA	ATTGTACTTT
2901	CTTTTGTGTC	TAATGATGTC	AAATACTTTT	TAAAATGTTT	ATTTTCAAT	CCATTACTTT	TTGAGAAATC	TCTGTTCACT	TCCATAGCCC	ATTTTGTCTG
3001	TTGTTTGTG	ACACAGGGTC	TTTCTCTATG	TATCCCTGGC	TATGCTGAGT	AGAGTTACCT	CAAAGCTGAC	AGAGATCCAT	CTACTTTTAC	CTCCAGGTCG
3101	CTGGGATTAG	AGGCATGACG	ATTTTAAAG	TTATTAATAT	TTATTTGTGT	ACCTGTGCTC	GATCTGTGTA	TGTGGATGGA	TGTTTGTCTT	GCCTGGATAG
3201	CTCTGCTCCA	CATGTGAGCC	AGTTACCTGC	GGTGGCCAGA	AGAGGGCATC	GGATGCCCTG	GAAGTGGAGT	TAGGATGGTT	GTGAGCTGCC	TGTGGGTGCT
3301	CGAACAACAG	CCTGGGTCTC	CGGGAGAGCA	GCGTTGTCTT	TACCTCCTAG	CCCACTCTCC	AGCTCCGGGG	GTGTATTCTT	GTCAAGAGA	CGCAGGAAGG
3401	CTCGAGCTTC	CCTCTTCTCC	GTGTAGACAT	CCAGTCTTCC	CAGCGCCAGT	TTGAGATGCT	CCCTCTCCCT	TCGTGATATT	TTGGTGTGTT	TTTCAAGAAAT
3501	CAGGTGGCTG	TAATGTATG	GCAATAGTCC	GGGTTTCCA	TTCTGTTGCA	CTGATCTACA	CACTGGTTTT	TGTGCCAGCA	CCGTGCCCTT	TGTTACCTCG
3601	ATTCTGTAGT	GTTATTTTGG	CTCAGAAATT	TTTTGGCTGC	CTGGGCCCTT	TGTGTTTTGC	ATCACTATT	CTACCGATCC	ATGAGCAGGG	AGACCTTTCA
3701	TCTACTAGTC	TCTGCCTTGA	TTTCTTTCTT	TAGAGTTTTT	TGAGACAGGG	TCTCACATAT	AATCTTGGCT	GACCAGGAAC	TCAGTGTGTA	GACCAGGCTG
3801	GCCTCAAAC	CACAGAGTTC	TGCTGCTCTC	TGCCCTCTGA	GTCTGGGGT	TTAAGGCTTA	TGCCACTGGG	CCTGGGATTT	TCTCTGATTT	TAAAGTTTTT
3901	ATTGTAGAGG	TTCTTCACTT	CTTTGCTTGG	GTTCCTCTG	AGGTACTTTG	TTTATTAAAG	GTCTATAAA	TGGGATTGTT	TTTCTGATTT	CTTCTTCAAC
4001	TTGTTTGCCA	TGGGATAAAA	AAAGCATGCC	ATGTGTGTAT	CCTGAGAAC	CAGAAGTGTT	AGTAAATCTA	GGAGCTTTCT	GGTGGAGACT	CTAGGCTCTC
4101	CCATGTACAG	CATTATATTC	TCTGTAGACA	GGAACACGCT	GTCTTCTTTA	TTTCTTACCT	ATATTCTTTT	CCCATCTTGT	TTTTATTGTT	TTAGCTAAGA
4201	CTAAAAACCC	AAATCGATGG	CCCTGTCTCG	CTTCTAGTTT	TAATGTGTAT	GTTTGTTTGG	CAGGGTCTCG	TTACTTAGCC	CAGGCTGGCC	TTGAATCTTT
4301	CCTGCTTCAT	CCAAACCCAGT	GCTGGGATTA	CCAGTACACA	GGAATCTATA	AAAAGGTTTT	TGTTTTTGT	ATTGTTTTTA	TTTCTCTCTT	CTCTGACTC
4401	ACATTGCCCT	TCTGTGTGCT	GAGATCATGC	CAGAGTCTCG	TGTGTGCTGG	GCAATTAGTG	ACCACTGAGC	TGGATCCCA	GTCCCTGTGT	TAATCAATG
4501	CCAAGTTTCA	TCCCATGCTC	TCAGCTCTCC	AGCATTCCAA	AGGAATTTGG	GGAAACAGAG	ATATGTAAAG	GAAACTGGAT	GTATTTACAA	TTTTAGGTAA
4601	ACAGATATGA	GGAAAAGGTT	TTGGGTTTCT	TCTAGACGTT	CCTGAGTCAG	GGTTTACATG	TGGCTAGGAC	CCAGCCGTGA	GGCTTTCTGT	GAGGATGCTG
4701	TTCTCTGTGC	TCATACTTCA	AACTAGGATG	GAAGCTCTGT	GGCCAACTCT	AGCTGTCTCAC	TTCTCTCTTT	TCGGCTCTGT	CCAGTCTTAT	GCTAGGTTTG
4801	CTATAAAGC	TCTAAATATT	AGAGAAATTA	AACAGAAAGT	GCTAGGCGTG	CCATTGCT				4858

Fig 22B

1	10	20	30	40	50	60	70	80	90	100
1	GTAGCACCTC	ACATACTCTC	CCAGCTCCAG	AGCTAGGCCC	CTCCTGGGGA	ATCACTGTTG	TACACTTCTT	TTCTGAGGG	ACTGTGCTGA	CATGTCTGAC
101	TGGGCTAGAG	AAATGTCTCA	CCACCCCTGG	TCCCATAGCA	TCCCTCACC	TGAGGTTGTC	ACAGGTAAGA	AAACCAGAAG	GCATCGAATT	AAATCCAGAG
201	GTGTAAAAGT	CAGGAGGAGT	TGTGTGAGAG	CTCACACCTG	TAATCTCAGC	ACACTGGGGG	AGAGGGACTG	CTTTGAGTTT	GAGGCCATCT	TGAGTGCTAT
301	ACATGGCAAG	TTCTGGGTCA	GCTTGGGTTA	GAGCAAGACC	TTTTCTAGGC	AAAGCAAGAC	ATTAGTCAGA	AGAACCAGT	CTCAGAGCTG	GACTTCGGGT
401	TTTATTGTTT	TGTTTGTGTT	TTTTTATTTT	TTGAGACAGG	GTTCCTCTGT	GTAGCCCTGG	TTGTCTGTGC	ACTCACTTTG	TAGACCAGAG	TGGCCTCGAA
501	CTCAGAAATC	TGCTTGCCTC	TGCCTCCGGA	GTGCTGGGAT	TAAAGGTGTG	CGCCACCACT	GCCTGGCTTA	GACTTCAAGT	TTTAAAGGCC	TAGAGTTGTA
601	GTTTGTAAAT	AAAGATCTGC	ATTGAGAACT	TGTGAGGCTG	AGGCAGGAAG	ACTGTGAGGT	CAGCCTGGCC	TTCAAGTGA	GTTTCAGGTC	AGCCTGAGAT
701	AGAGGAGCAG	TGTGAGGCCA	GAAGGACCCC	ACAAAGAAAG	ACCTCCACAG	CGCTGCTTCT	AACGGGTCCA	GCTTCGAGAG	GCTTCTCAC	AGCTGCCAGA
801	GAGAATGTTG	TTGGCCCTCT	GAGGAGATAG	AGTGATAGTG	ACTCTGTGTG	TGTGTGTGTA	AATATATACT	GTATATACTG	TGAGGGTGCA	TGTGTGCAAC
901	ATGCATATGT	ACTGTGAAAA	TGTGTGAGAG	GCAGTGTGTT	CGTATGTGTG	TCTGTGAGTA	TAACCATATG	GTATGTAATC	T	981

Fig 23

Triple-lox vectors for loxP/Cre targeted deletion

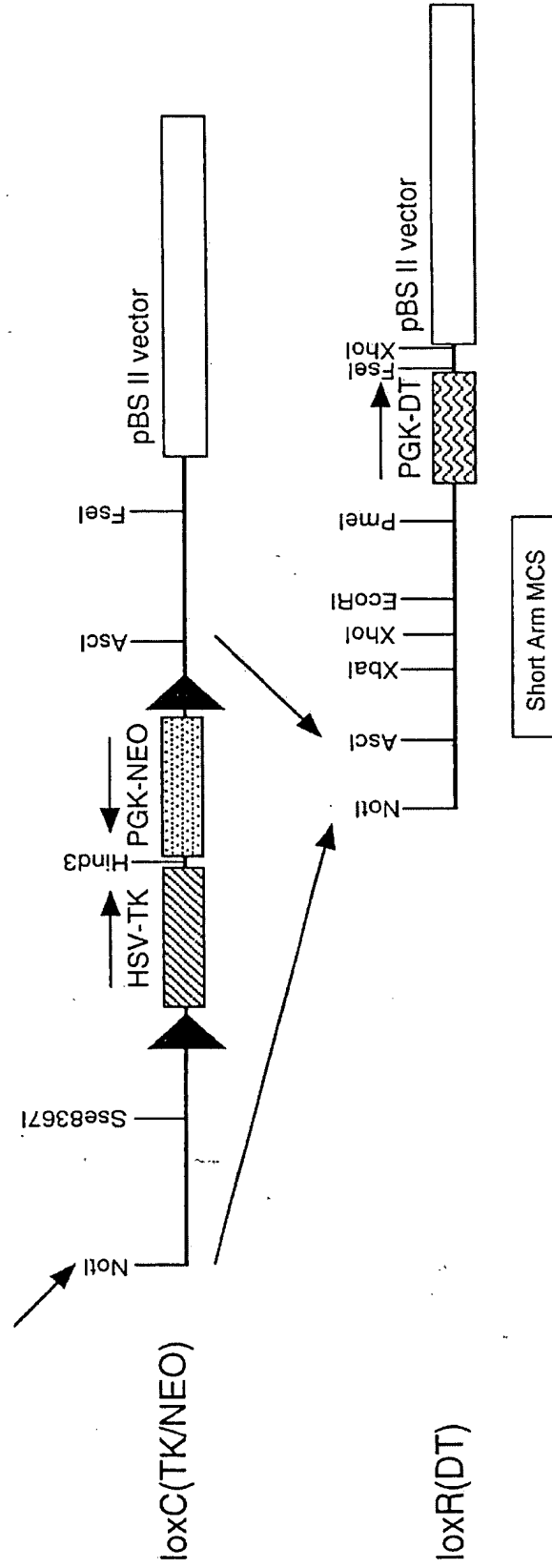


Fig 24

Structural motif involved in binding lithium

